

## FIG. 1

```

-54  AGCTGCGGCCCGGTCTGCCAGCCAGACCCTTTGGAGAAGACCCCACTCCCTGTC
1  ATGGGCCCCCGCTGCACCCTGCACCCOCTTTCTCTCCTGGTGCAGGTGACAGCGCTGGCT 60
   M G P R C T L H P L S L L V Q V T A L A
61  GCGACTCTGGCCCAGGGCAGGCTGCCTGCCTTCCTGCCCTGTGAGCTCCAGCCCCACGGC 120
   A T L A Q G R L P A F L P C E L Q P H G
121 CTGGTGAAGTGCAGTGGCTCTTCCTGAAGTCCGTGCCCCACTTCTCGGCGGCAGCGCC 180
   L V N C N W L F L K S V P H F S A A A P
181 CGGGCCAACGTCAACAGCCTCTCCTTACTCTCCAACCGCATCCACCACTTGCACGACTCT 240
   R A N V T S L S L L S N R I H H L H D S
241 GACTTGGTCCACCTGTCCAGCCTACGAACTCTCAACCTCAAGTGGAACTGCCCGCOGGCT 300
   D F V H L S S L R T L N L K W N C P P A
301 GGCCTCAGCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAACACCTTCCTGGCC 360
   G L S P M H F P C H M T I E P N T F L A
361 GTGCCCACCCTGGAGGAGCTGAACCTGAGCTACAACAGCATCAGACCGTGCTGCCCCTG 420
   V P T L E E L N L S Y N S I T T V P A L
421 CCCGACTCCCTCGTGTCCCTGTGCTGAGCGGCACCAACATCCTGGTGCTAGACCCOACC 480
   P D S L V S L S L S R T N I L V L D P T
481 CACCTCACTGGCCTACATGCCCTGCGCTACCTGTACATGGATGGCAACTGCTACTACAAG 540
   H L T G L H A L R Y L Y M D G N C Y Y K
541 AACCCCTGCCAGGGGGCGCTGGAGGTGGTGCCGGGTGCCCTCCTCGGCCTGGGCAACCTC 600
   N P C Q G A L E V V P G A L L G L G N L
601 ACACATCTCTCACTCAAGTACAACAATCTCACGGAGGTGCCCGCAGCCTGCCCCCAGC 660
   T H L S L K Y N N L T E V P R S L P P S
661 CTGGAGACCCTGCTGTTGTCCTACAACCACATTGTCACCCTGACGCTGAGGACCTGGCC 720
   L E T L L L S Y N H I V T L T P E D L A
721 AATCTGACTGCCCTGCGCGTGCTTGATGTGGGGGGGAAGTCCCGCGCTGTGACCATGCC 780
   N L T A L R V L D V G G N C R R C D H A

```

## FIG. 2

781 OGCAACCCCTGCAGGGAGTGCCCAAAGGACCACCCCAAGCTGCACTCTGACACCTTCAGC 840  
R N P C R E C P K D H P K L H S D T F S  
841 CACCTGAGCCGCCTCGAAGGCCTGGTGTGAAAGACAGTTCTCTCTACAACCTGGACGCC 900  
H L S R L E G L V L K D S S L Y N L D A  
901 AGGTGGTTCCGAGGCCTGGACAGGCTCCAAGTGCTGGACCTGAGTGAGAACTTCCTCTAC 960  
R W F R G L D R L Q V L D L S E N F L Y  
961 GACTGCATCACCAAGACCACGGCCTTCCAGGGCCTGGCCCGACTgCGcAAGCTCAACCTG 1020  
D C I T K T T A F Q G L A R L R K L N L  
1021 TCCTTCAATTACCACAAGAAGGTGTCTTTGCCACCTGCACCTGGCACCTTCCTTTGGG 1080  
S F N Y H K K V S F A H L H L A P S F G  
1081 CACCTCCGGTCCCTGAAGGAGCTGGACATGCATGGCATCTTCTTCCGCTCGCTCAGTGAG 1140  
H L R S L K E L D M H G I F F R S L S E  
1141 ACCACGCTCCAACCTCTGGTCCAAGTGCCTATGCTCCAGACCCCTGGCCTGCAGATGAAC 1200  
T T L Q P L V Q L P M L Q T L R L Q M N  
1201 TTCATTAACCAGGCCCAGCTCAGCATCTTTGGGGCCTTCCCTGGCCTGCTGTACGTGGAC 1260  
F I N Q A Q L S I F G A F P G L L Y V D  
1261 CTATCGGACAACCGCATCAGCGGAGCTGCAAGGCCAGTGGcCATTACTAGGGAGGTGGAT 1320  
L S D N R I S G A A R P V A I T R E V D  
1321 GGTAGGGAGAGGGTCTGGCTGCCTTCCAGGAACCTCGCTCCACGTCCACTGGACACTCTC 1380  
G R E R V W L P S R N L A P R P L D T L  
1381 CGCTCAGAGGACTTCATGCCAAACTGCAAGGCCTTCAGCTTCACCTTGGACCTGTCTCGG 1440  
R S E D F M P N C K A F S F T L D L S R  
1441 AACAACTGGTGACAATCCAGTCGGAGATGTTTGCTCGCCTCTCAGCCTOGAGTGCCTG 1500  
N N L V T I Q S E M F A R L S R L E C L  
1501 CGTCTGAGCCACAACAGCATCTCCAGGCGGTCAATGGCTCTCAGTTTGTGCCGCTGACC 1560  
R L S H N S I S Q A V N G S Q F V P L T

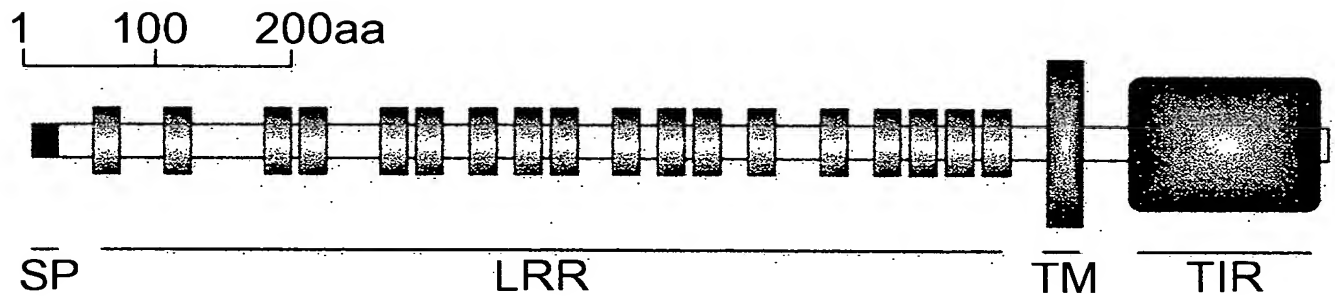
## FIG. 3

1561 AGCCTGCGGGTGCTGGACCTGTCCACAACAAGCTGGACCTGTATCACGGGCGCTCGTTC 1620  
S L R V L D L S H N K L D L Y H G R S F  
1621 ACGGAGCTGCCGCGCCTGGAAGCACTGGACCTCAGCTACAACAGCCAGCCCTTTACCATG 1680  
T E L P R L E A L D L S Y N S Q P F T M  
1681 CAGGGTGTGGGCCACAACCTCAGCTTCGTGGGCCAGCTGCCCGCCCTGCGCTACCTCAGC 1740  
Q G V G H N L S F V A Q L P A L R Y L S  
1741 CTGGCGCACAATGACATCCATAGCCGAGTGTCCAGCAGCTCTGTAGCGCCTCACTGTGC 1800  
L A H N D I H S R V S Q Q L C S A S L C  
1801 GCCCTGGACTTTAGCGGCAACGATCTGAGCCGGATGTGGGCTGAGGGAGACCTCTATCTC 1860  
A L D F S G N D L S R M W A E G D L Y L  
1861 CGCTTCTTCCAAGGCCTAAGAAGCCTAGTCTGGCTGGACCTGTCCCAGAACCACCTGCAC 1920  
R F F Q G L R S L V W L D L S Q N H L H  
1921 ACCCTCCTGCCACGTGCCCTGGACAACCTCCOCAAAGCCTGAAGCATCTGCATCTCCGT 1980  
T L L P R A L D N L P K S L K H L H L R  
1981 GACAATAACCTGGCCTTCTTCAACTGGAGCAGCCTGACCCTCCTGCCCAAGCTGGAAACC 2040  
D N N L A F F N W S S L T L L P K L E T  
2041 CTGGACTTGGCTGGAAACCAGCTGAAGGOCCTAAGCAATGGCAGCCTGCCATCTGGCAOC 2100  
L D L A G N Q L K A L S N G S L P S G T  
2101 CAGCTGCGGAGGCTGGACCTCAGTGGCAACAGCATCGGCTTTGTGAACCTGGCTTCTTT 2160  
Q L R R L D L S G N S I G F V N P G F F  
2161 GCCCTGCCCAAGCAGTTAGAAGAGCTCAACCTCAGCGCCAATGCCCTCAAGACAGTGGAG 2220  
A L A K Q L E E L N L S A N A L K T V E  
2221 CCTCCTGGTTTGGCTCGATGGTGGGCAACCTGAAAGTCCTAGACGTGAGCGCCAACCCT 2280  
P S W F G S M V G N L K V L D V S A N P  
2281 CTGCACTGCGCCTGTGGGGCGACCTTCGTGGGCTTCCTGCTGGAGGTACAGGCTGCGGTG 2340  
L H C A C G A T F V G F L L E V Q A A V

## FIG. 4

2341 CCTGGGCTGCCCAGCCGCGTCAAGTGTGGCAGTCCGGGGCAGCTCCAGGGCCATAGCATC 2400  
 P G L P S R V K C G S P G Q L Q G H S I  
 2401 TTTGCGCAAGACCTGCGCCTCTGCOCTGGATGAGACCOCTCTCGTGGAAGTGT TTTGGCATC 2460  
 F A Q D L R L C L D E T L S W N C F G I  
 2461 TCGCTGCTGGCCATGGOCCTGGGCOCTGGTTGTGOCATGCTGCACCACCTCTGCGGCTGG 2520  
S L L A M A L G L V V P M L H H L C G W  
 2521 GACCTCTGGTACTGCTTCCACCTGIGCOCTGGCOCTGGCTGCCCCACCGAGGGCAGCGGCGG 2580  
 D L W Y C F H L C L A W L P H R G Q R R  
 2581 GCGCAGACGCCCTGTTCTATGATGCCTTCGTGGTCTTTGACAAAGCTCAGAGTGCTGTG 2640  
 G A D A L F Y D A F V V F D K A Q S A V  
 2641 GOCGACTGGGTGTACAACGAGCTGCGGGTGCAGCTGGAGGAGCGCCGTGGGOGCCgCGCA 2700  
 A D W V Y N E L R V Q L E E R R G R R A  
 2701 CTGCGCCTGTGCOCTGGAGGAGCGAGACTGGTTACCTGGCAAGACGCTCTTCGAGAACTG 2760  
 L R L C L E E R D W L P G K T L F E N L  
 2761 TGGGCCTCAGTCTACAGCAGCCGCAAGACCOCTGTTTGTGCTGGCCACACGGACCGTGTC 2820  
 W A S V Y S S R K T L F V L A H T D R V  
 2821 AGCGCCCTCTTGCGTGCCAGTTTCTGCTGGCCAGCAGCGCOCTGCTGGAGGACCGCAAG 2880  
 S G L L R A S F L L A Q Q R L L E D R K  
 2881 GACGTTGTAGTGCTGGTGATCCTGCGCCCCGATGCCTACCGCTCCCGCTACGTGCGGCTG 2940  
 D V V V L V I L R P D A Y R S R Y V R L  
 2941 CGCCAgCGCCTCTGCCGCCAGAGTGTOCTCCTCTGGCCCCACCAGCCCOGTGGGCAGGGC 3000  
 R Q R L C R Q S V L L W P H Q P R G Q G  
 3001 AGCTTCTGGGCCAGCTGGGCACAGCOCTGACCAGGGACAACCGCCACTTCTATAACCGG 3060  
 S F W A Q L G T A L T R D N R H F Y N R  
 3061 AACTTCTGCCGGGGCCCCACGACAGCCGAATAG 3093  
 N F C R G P T T A E \*

FIG. 5



## FIG. 6

SWINE	1	MCPRCT--LHPLSLLVQVTLAATLAQGRLPAFLPCELOPHGLVNCNWFLKSVPHFSAA	58	SWINE
HUMAN	1	MCF-CRSALHPLSLLVQAIMLAMTLALGTLPALPCELOPHGLVNCNWFLKSVPHFSMA	59	HUMAN
MOUSE	1	MVLRRT-LHPLSLLVQAAVLAETLALGTLPALPCELPKPHGLVDCNWFLKSVPRFSAA	59	MOUSE
CAT	1	MCF-CHGALHPLSLLVQAAALAVALAQGTLPALPCELOPHGLVNCNWFLKSVPHFSAA	59	CAT
* . . . . . ***** . ** . ** * . ***** . . ***** . * . ***** . ** . *				
SWINE	59	APRANVTLSLLSNRIHHLHDSDFVHLSSLRTNLKWNCPAGLSPMHFPCHMTIEPNTF	118	SWINE
HUMAN	60	APRGVNTLSLSSNRIHHLHDSDFVHLPSLRHNLKWNCPVGLSPMHFPCHMTIEPSTF	119	HUMAN
MOUSE	60	ASCSNITRLSLISNRIHHLHNSDFVHLNLRLQNLKWNCPPTGLSPLHFSCHMTIEPRTF	119	MOUSE
CAT	60	APRGVNTLSLSLYSNRIHHLHDSDFVHLSSLRRNLKWNCPASLSPMHFPCHMTIEPHTF	119	CAT
* . . * . * . *** . ***** . *** . * . * . ***** . *** . * . ***** . **				
SWINE	119	IAVPTLEEINLSYNSITTVPALPDSLSLSLRTNIVLDPTHLTGLHALRYLYMDGNCY	178	SWINE
HUMAN	120	IAVPTLEEINLSYNNIMTVPALPKSLISLSLSHTNIMLDSASLAGLHALRFLFMDGNCY	179	HUMAN
MOUSE	120	IAMPTELEEINLSYNGITTVPRLPSSLVNLSSHTNIVLDANSIAGLYSLRVLFMDGNCY	179	MOUSE
CAT	120	IAVPTLEEINLSYNSITTVPALPSSLVLSLSRTNIVLDPANLAGLSLRFILFDGNCY	179	CAT
** . . ***** * . *** . * . * . ***** . * . * . * . * . *****				
SWINE	179	YKNPCQGALEVPGALLGLGNLTHLSLKYNNTLTVPRSLPPSLETLLLSYNHIVTLTPED	238	SWINE
HUMAN	180	YKNPCQGALEVPAGALLGLGNLTHLSLKYNNTLTVPRNLPSSEYLLLSYNRIVKLAPED	239	HUMAN
MOUSE	180	YKNPCTGAVKVPAGALLGLSNLTHLSLKYNNTLTVPRQLPPSLEYLLVSYNLIVKLGPED	239	MOUSE
CAT	180	YKNPCQALQVAPGALLGLGNLTHLSLKYNNTLTVPRGLPPSLEYLLLSYNHIITLAPED	239	CAT
***** * . * . ***** . ***** . ***** . * . * . * . * . *****				
SWINE	239	LANLTALRVLDVGGNCRRCDHARNPCRECPKDHPLHSDTFSHLSRLEGLVLKDSSLYNL	298	
HUMAN	240	LANLTALRVLDVGGNCRRCDHAPNPMCECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWL	299	
MOUSE	240	LANLTSLRVLDVGGNCRRCDHAPNPCIECGQSLHLPETFHLSHLEGLVLKDSSLHTL	299	
CAT	240	LANLTALRVLDVGGNCRRCDHARNPMCECPKGFPHLPDTFSHLNHLEGLVLKDSSLYNL	299	
***** . ***** . ***** . ***** . * . * . * . * . ***** . *				

## FIG. 7

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SWINE 299 DARWFRGLDRLOVLDLSENFYDCITKTTAFQGLARLRKLNLSFNHYHKKVSFAHLHLAPS 358
HUMAN 300 NASWFRGLGNLRVLDLSENFYKCTIKTKAFQGLTQLRKLNLSFNHYQKRVSFHLSLAPS 359
MOUSE 300 NSSWFQGLVNLSVLDLSENFYESIINHINAFQNLTRLRKLNLSFNHYRKKVSFARLHLASS 359
CAT 300 NPRWFHALGNLMVLDLSENFYDCITKTTAFQGLAQLRRRLNLSFNHYHKKVSFAHLHLAPS 359
      .  ** . * . * ***** . . . * * * . * ** ***** * . * * * . * . * . *
SWINE 359 FGHLSRLKELDMHGIFFRSLSETTLQPLVOLPMLQTLRLQMFINQAQLSIFGAFFPGLLY 418
HUMAN 360 FGSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMFINQAQLGIFRAFFPGLRY 419
MOUSE 360 FKNLVSLQELNMHGIFFRSLNKYTLRWLADLPKLHTLHLQMFINQAQLSIFGTFRALRF 419
CAT 360 FGSLLSLQQLDMHGIFFRSLSETTLRSLVHLPMQLSHLQMFINQAQLSIFGAFFPGLRY 419
      * . * . * . * . * ***** . . * . * * . * . * ***** . * . * . * . .
SWINE 419 VDLSDNRI SGAARPVAITREVDGR-ERVWLPSRNLAPRPLDTLRSEDFMPNCKAFSFTLD 477
HUMAN 420 VDLSDNRI SGASELTATMGEADGG-EKVLWQPGDLAPAPVDTPSSEDFRPN CSTLNFTLD 478
MOUSE 420 VDLSDNRI SGPSTLSEATPEEADDAEQEELLSADPHAPLSTPASKNFMORCKNFKFTMD 479
CAT 420 VDLSDNRI SGAMELAAATGEVDGG-ERVRLPSGDLALGPPGTPSSEGFMPGCKTLNFTLD 478
      ***** . . . . * .. * . * . . . . * * . * . * . * . * . *
SWINE 478 LSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVLDLSHNKLDLYHG 537
HUMAN 479 LSRNNLVTIQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSRNKLDLYHE 538
MOUSE 480 LSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLTNLQVLDLSHNKLDLYHW 539
CAT 479 LSRNNLVTIQPEMFARLSRLQCLLSRNSISQAVNGSQFMPLTSLQVLDLSHNKLDLYHG 538
      ***** . . . * * . * . * * * . * . * . * . * . * . * . * . * . *

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## FIG. 8

SWINE	538	RSFTELPRLAALDLSYNSQPFIMQGVGHNLSEVAQLPALRYLSLAHNDIHSRVSQQLCSA	597
HUMAN	539	HSFTELPRLAALDLSYNSQPFIMQGVGHNLSEVAHLRTLRLSLAHNNIHSQVSOQLCST	598
MOUSE	540	KSFSELPQLQALDLGYSQPFISIKGIGHNLSEVAHLSMLHSLSLAHNDIHTRVSSHLSNS	599
CAT	539	RSFTELPRLAALDLSYNSQPFIMQGVGHNLSEVAQLPALRYLSLAHNDIHSRVSQQLCSA	598
** .*** .* .***** .***** ..* .*** ***** * * .***** .** ..** .* .*			
SWINE	598	SLCALDFSGNDLSRMWAEGDLYLRFFQGLRSLVWLDLSQNLHTLLPRALDNLPKSLKHL	657
HUMAN	599	SLRALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNLHTLLPQTLRNLPKSLQVL	658
MOUSE	600	SVRFILDFSGNGMGRMWDEGGLYLHFFQGLSGLLKLDLSQNLHLLRPQNLNLPKSLKLL	659
CAT	599	SLRALDFSGNALSRMWAEGDLYLKFFRGLRSLVRLDSLQNLHTLLPRTLNLPKSLRLL	658
*...***** . .**.*.*** **.* * ***** **.* * .***** *			
SWINE	658	HLRDNLAFFNWSSLTLLPKLETLDLAGNQLKALSNGSLPSGTQLRRDLSGNSIGFVNP	717
HUMAN	659	RLRDNLAFFKWSLHFLPKLEVLDLAGNRLKALINGSLPAGTLRRDLVSCNSISFVAP	718
MOUSE	660	SLRDNLSFFNWTSLSFLPNLEVLDLAGNQLKALINGTLPNGTLQKLDVSSNSIVSVVP	719
CAT	659	RLRDNLAFFNWSSLVLLPRLAALDLAGNQLKALSNGSLPNGTQLQRLDSSNSISFVAS	718
**** .* .**.* ** ** ***** .***** **.* ** * .**.* *** .* .			
SWINE	718	GFFALAKQLEELNLSANALKTVEPSWFGSMVGNLKVLDVSNPLHCACGATFVGFLLLEVQ	777
HUMAN	719	GFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSNPLHCACGAAFMDFLLLEVQ	778
MOUSE	720	AFFALAVELKEVNLSHNILKTVDRSWFGPIVMNLTVLDVRSNPLHCACGAAFVDLLLEVQ	779
CAT	719	SFFALATRLRELNLSANALKTVEPSWFGSLAGTLKVLDVTGNPLHCACGAAFVDFLLLEVQ	778
**.* * * .*** .* .***** ***** * .*** ***** .*...*****			
SWINE	778	AAVPGLPSRVKCGSPGQLQGHISIFAQDLRLCLDETLSWNCFGISLLAMALGLVVPMLHHL	837
HUMAN	779	AAVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLVPMPLHHL	838
MOUSE	780	TKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFGLSLLAVAVGMVPMPLHHL	839
CAT	779	AAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFGLSLLTVALGLAVPMPLHHL	838
..**** . ***** ***** ***** *** .** ..*** .* .* .**.*			



## FIG. 9

SWINE	838	CGWDLWYCFHLCLAWLPHRGQRRGAD--ALFYDAFVFDKAQSAVADWVYNEIRVQLEER	895
HUMAN	839	CGWDLWYCFHLCLAWLPWRGQSCGRDEDALPYDAFVFDKTQSAVADWVYNEIRGQLEEC	898
MOUSE	840	CGWDVWYCFHLCLAWLPLIARSRRSAQA-LPYDAFVFDKAQSAVADWVYNEIRVRLEGR	898
CAT	839	CGWDLWYCFHLCLAWLPRGRRRRGAD--ALPYDAFVFDKAQSAVADWVYNEIRVRLEER	896
**** . ***** . . . . . * . ***** . ***** . **..			
SWINE	896	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFLLAQORL	955
HUMAN	899	RGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQORL	958
MOUSE	899	RGRRALRLCLEERDWLPGQTLFENLWASTYGSRKTLFVLAHTDRVSGLLRTSFLLAQORL	958
CAT	897	RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQORL	956
*** . ***** . ***** . ***** . * *** . ***** . *****			
SWINE	956	LEDKDVVVLVILRPDAYRSRYVRLRQRLCRQSVLLWPHQPRGQGSFWAQLGTALTRDNR	1015
HUMAN	959	LEDKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQGSFWAQLGMALTRDNH	1018
MOUSE	959	LEDKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLFWPQPNQGGGFWAQLSTALTRDNR	1018
CAT	957	LEDKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLLWPHQPSGQGSFWAQLGTALTRDNQ	1016
***** . ** . ***** . ** . ** . ***** . *****			
SWINE	1016	HFYNRNFCRGPTTAE	1030
HUMAN	1019	HFYNRNFCQGP-TAE	1032
MOUSE	1019	HFYNQNFRCGP-TAE	1032
CAT	1017	HFYNQNFRCGPTTAE	1031
***** *** . ** ***			

FIG. 10

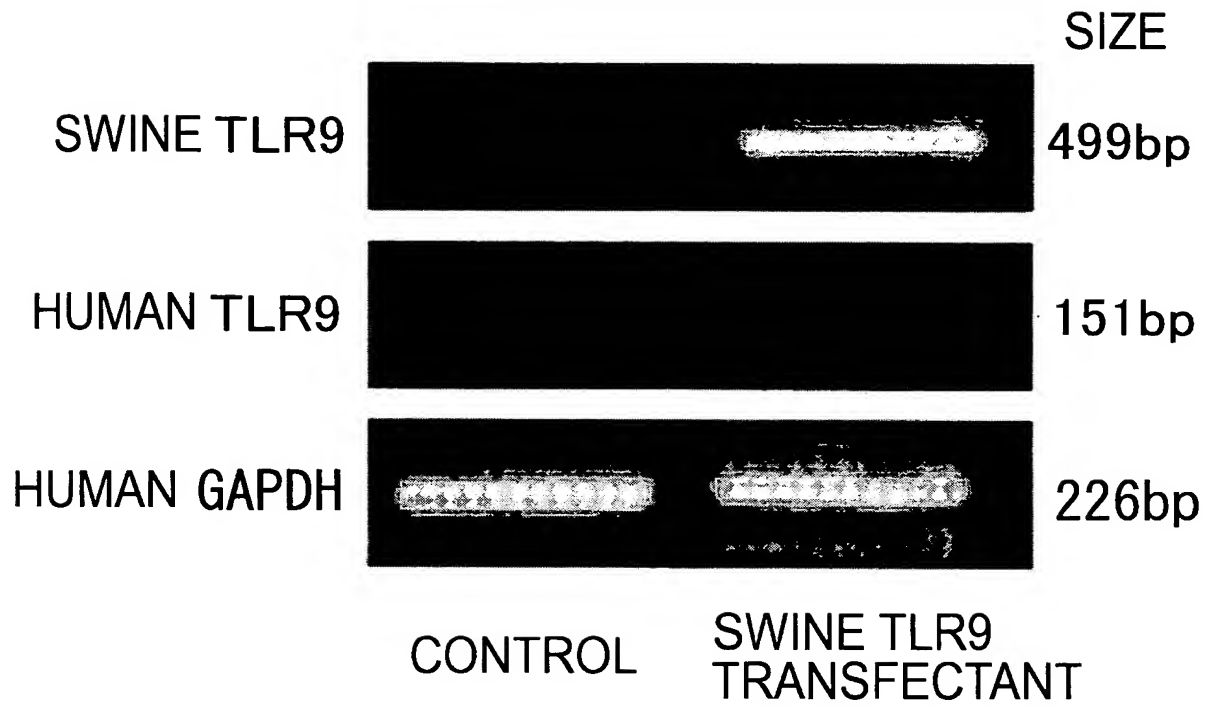


FIG. 11

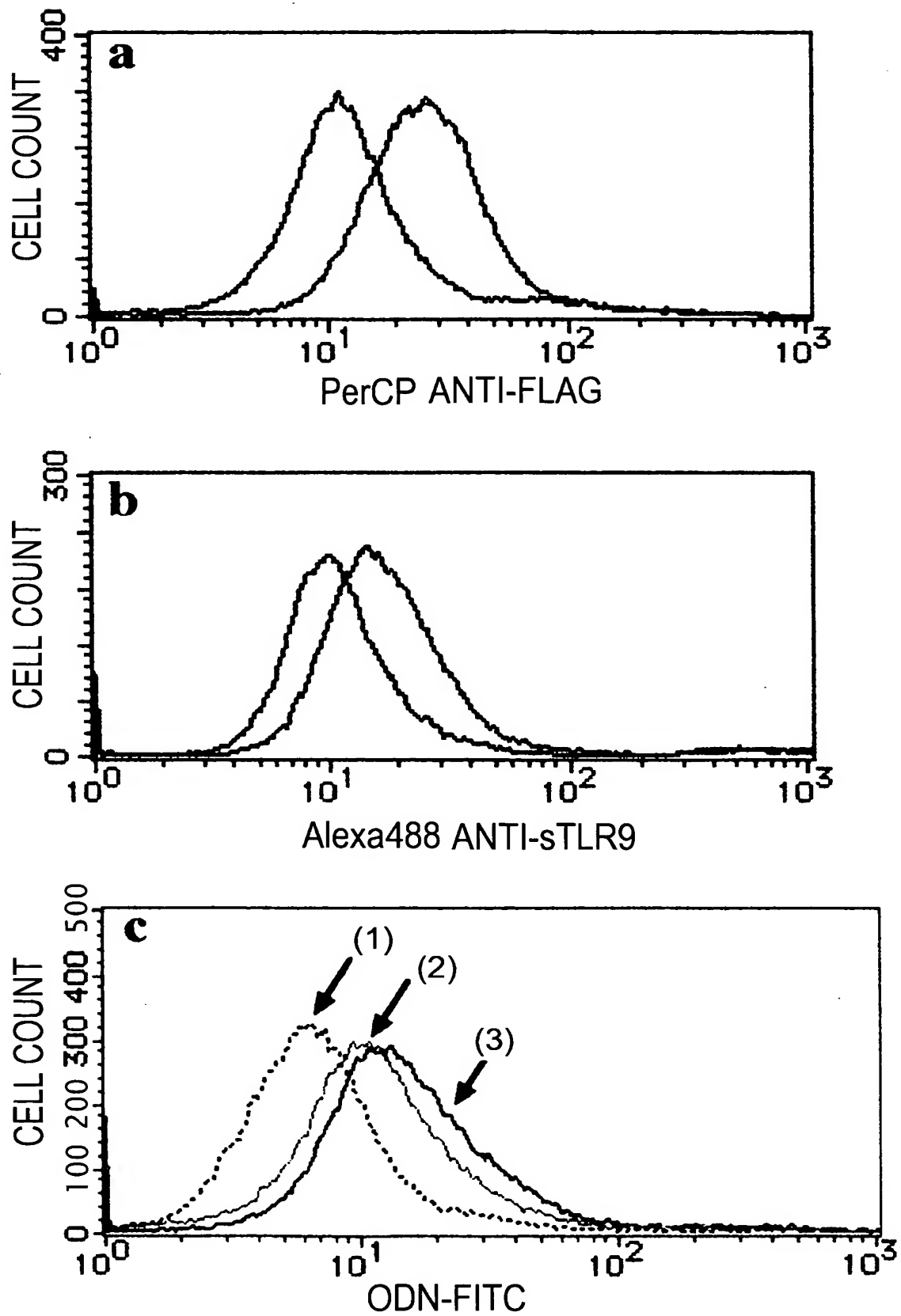


FIG. 12

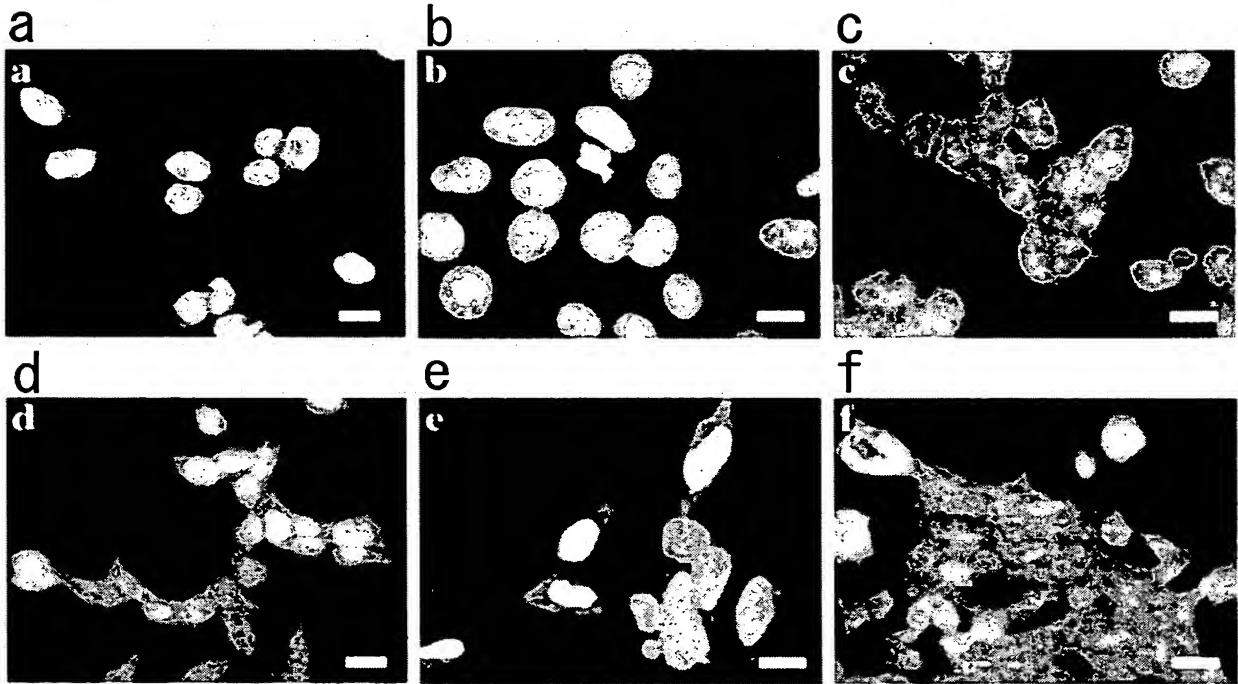


FIG. 13

